

BEST AVAILABLE COPY

CCACGGGTCCGAGAAATTGAAAGGGTGCCCAAGGACAATCTCTAAAGGGGTAAGGGACATACCTACCITGTCGGT
 AGGGGAGATGTTTCGTTTTTCATGCTTTACCAGAAAATCGACTTCCTCCCGACCTTAGTTTCAAGCTTATTCCTTAATT
 AGAGACAAGAAACCTCTTTCAACTTGAAGACACCGTATGAGGTGAAATGGACACCCAGCCACCACAATGAAGAAATCAA
 ACCAGGAATACCTATGCTGAACCCAGGCTCAATCGTCCCGAGTGTTCCTGACACCGCATCTTTGCTTACAGTGCAT

H G F N L T L A K L P N N E L H	16
CACAACTGAAGA ATG GGG TTC AAC TTG AGC CTT GCA AAA TTA CCA AAT AAC GAG CTG CAC	48
G Q E S H N S G N R S D G P G K N T T L	36
GGC CAA GAG AGT CAC AAT TCA GGC AAC AGC AGC GAG GGG CCA GGA AAG AAC ACC ACC CTT	108
H N E F D T I V L P V L Y L I I F V A S	56
CAC AAT GAA TTT GAC ACA ATT GTC TTG CCG GTC CTT TAT CTC ACT ATA TTT GTG GCA AGC	168
I L L N G L A V W I F P H I R N K T S P	76
ATC TTG CTG AAT GGT TTA GCA GTG TGG ATC TTC TTC CAC ATT AGG AAT AAA ACC AGC TTC	228
I F Y L K N I V V A D L I M T L T F P F	96
ATA TTC TAT CTC AAA AAC ATA GTC GTT CCA GAC CTC ATA ATG ACG CTC ACA TTT CCA TTT	288
R I V H D A G F G P W Y F K F I L C R V	116
CCA ATA GTC CAT GAT CCA GGA TTT GGA CCT TGG TAC TTC AAG TTT ATT CTC TGC AGA TAC	348
T S V L F Y A N M Y T S I V F L G L I S	136
ACT TCA CTT TTG TTT TAT CCA AAC ATG TAT ACT TCC ATC GTG TTC CTT GGG CTG ATA AGC	408
I D R Y L K V V K P F G D S R M Y S I T	156
ATT GAT CCG TAT CTG AAG GTG GTC AAG CCA TTT GGG GAC TCT CGG ATG TAC AGC ATA ACC	468
F T K V L S V C V W V I M A V L S L P N	176
TTC ACG AAG GTT TTA TCT GTT TGT CTT TGG GTG ATC ATG GCT GTT TTG TCT TTG CCA AAC	528
I I L T N G Q P T E D N I H D C S K L K	196
ATC ATC CTG ACA AAT GGT CAG CCA ACA GAG GAC AAT ATC CAT GAC TGC TCA AAA CTT AAA	588
S P L G V K W H T A V T Y V N S C L F V	216
AGT CCT TTG GGG GTC AAA TGG CAT ACG CCA GTC AGC TAT GTG AAC AGC TGG TTG TTT GTG	648
A V L V I I G C Y I A I S R Y I H K S	236
GCC GTG CTG GTG ATT CTG ATC GGA TGT TAC ATA GCC ATA TCC AGG TAC ATC CAC AAA TCC	708
S R Q F I S Q S S R K R K H N Q S I R V	256
ACC AGG CAA TTC ATA AGT CAG TCA AGC CGA AAG CGA AAA CAT AAC CAG AGC ATC AGG GTT	768
V V A V F F T C F L P Y H L C R I P F T	276
GTT CTC CCT GTC TTT TTT ACC TGC TTT CTA CCA TAT CAC TTG TGC AGA ATT CCT TTT ACT	828
F S H L D R L L D E S A Q K I L Y Y C K	296
TTT AGT CAC TTA GAC AGG CTT TTA GAT GAA TCT GCA CAA AAA ATC CTA TAT TAC TGC AAA	888
E I T L F L S A C N V C L D P I I Y F F	316
GAA ATT ACA CTT TTC TTG TCT GCG TGT AAT GTT TGC CTC GAT CCA ATA ATT TAC TTT TTC	948
M C R S F S R R L F K K S N I R T R S E	336
ATG TGT AGG TCA TTT TCA AGA AGG CTG TTC AAA AAA TCA AAT ATC AGA ACC AGG AGT GAA	1008
S I R S L Q S V R R S E V R I Y Y D Y T	356
ACC ATC AGA TCA CTG CAA AGT GTG ACG AGA TCG GAA GTT CGC ATA TAT TAT GAT TAC ACT	1060
D V	359
GAT GTG TAG	1077

CCCTTTTATGTTTGTTCGAATCGATATGTACAAGCTGTAATAAATGTTTCTTTTCATTAAATAAATAAATAAATAA
 AAAAG

FIG 1

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Score: 133.33 Seq: 59 314 Model: 1 255

*GNILVIWVICRYRRMRTPMNYFIVNLAVADLLFslfcmPFWHVVYVKGQ
 N+L +W+++ R +T++ +++ N VADL++ ++T+P+ +V+ + G

#1h2871 59 LNGLAVWIFFHIRN-KTSFIFYLKNIVVADLIH-TLTFPFRIVHDAGFG 105

RWpFGdEMCrIwMYFDYMMNVASIFELTcISIDRYLWAIChPN-VmRvMT
 W+p ++CR ++ ++Y NMY+SI PL +ISIDRYL ---P+ R+ -

#1h2571 106 PWYFKFYLCRYTSVLFYANMYTSIVFLGLISIDRYL-KVVKPFGDSRMYS 154

pRHRAWVMIiIwVMSF1ISMPPFLMFWscyrDEnaWmTWCMiyDWPa
 +++ +-V++++WV++++S+P + + + + + E-N+ C+ - P

#1h2571 155 ITP-TKVLSTVCVWVMAVLSLP-N-II-LTNGQP-TEDNIDCSKLSFL 199

.WFWWVYVILmciimgFYIPNIIM1FCYWRIVRIaRIWVRNips>GpFR+
 + W - V--- - F- - I - CY I R +---R- S--

#1h2371 200 GYXWHTAVCYVNS-CLFVAVLVELIGCVIAISRYIXSSPQFISGES--- 245

msMRpERRIVKMiiIIMVVFIIcW1PYFIvMINDTLH.XWwFCeJC.IwF
 + R+R- - --- VF+ C+LPY++ + T- - -

#1h2571 246 ----RKRKHNSIRVVVAVVFTCFILPYHLCAIPFTPSHLDRLLD-ESACK 290

Flwm.Y.IfewLayVNCpCinPIIY
 +L++ I+++L+ +N C++PIIY

#1h2871 291 ILVYCKEITLFLSACIV-CLDPIIY 314

FIG 2

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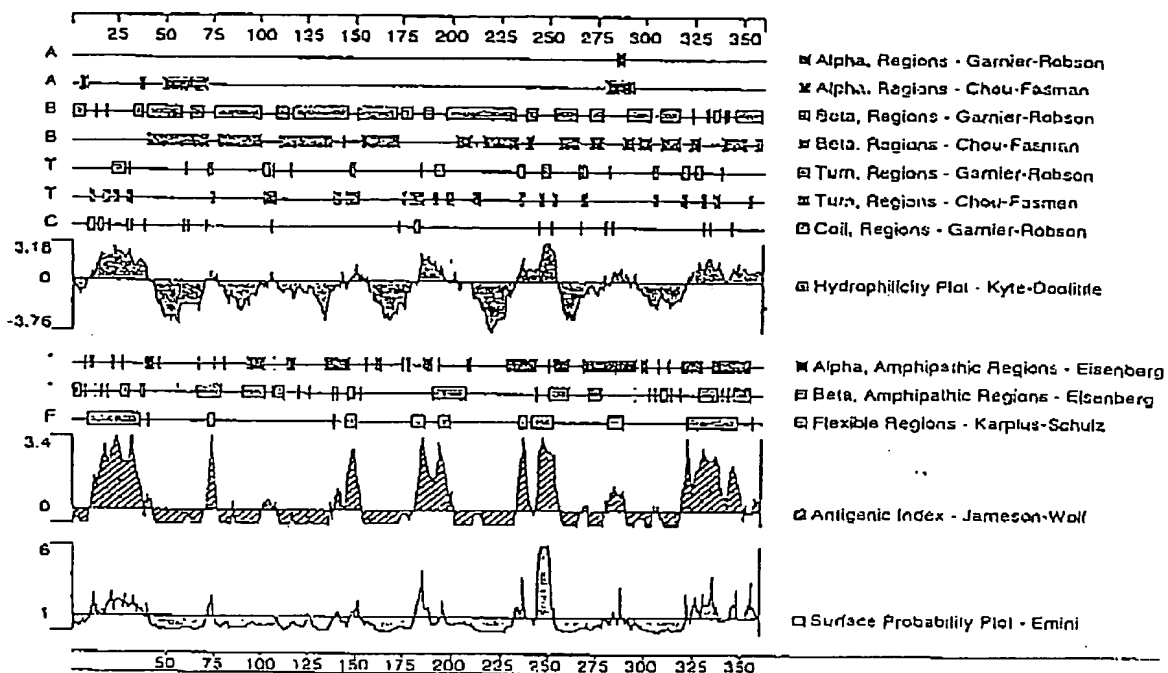


FIG 3

66050" 5442E60

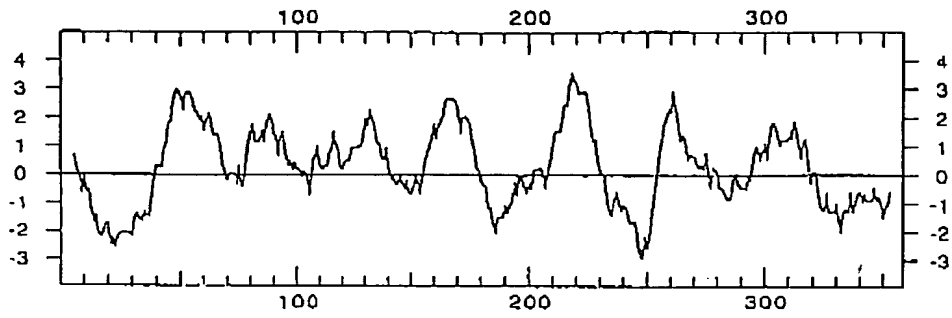
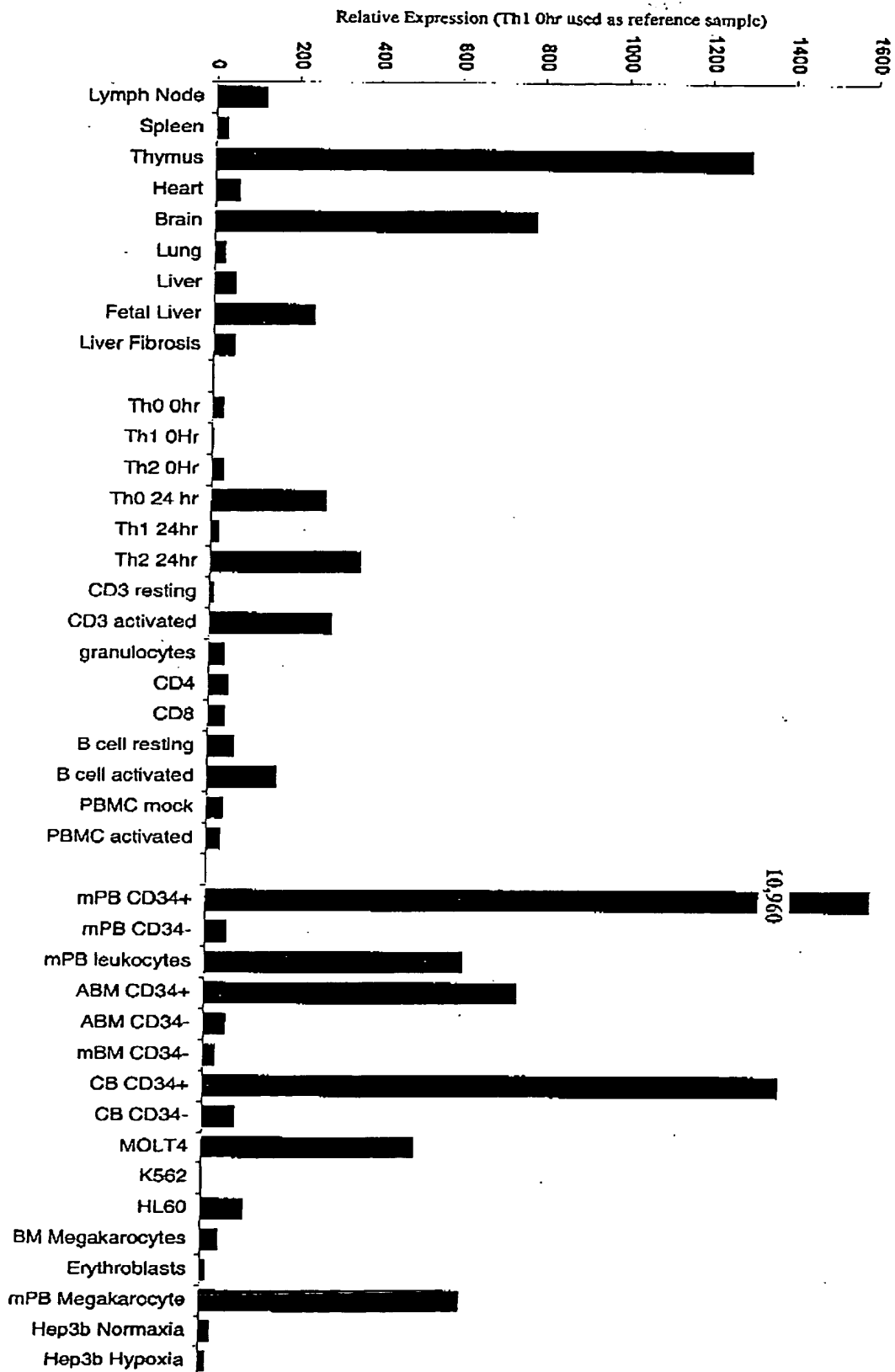


FIG 4

LEGAL DEPT.



2871 Expression

FIG 5

00324455 050299